**University of Leicester**

**MIBTP studentship project 2026**

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| **Additional Supervisor** |  |

**Section 2 – *Project Information***

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| **Project Title** | Using resurrected crustaceans to understand how ancestral exposure to pollution affects epigenetic biomarkers of transgenerational health. |
| **Project Summary** | |
| Environmental insults such as pollution can cause transgenerational negative  health outcomes in both wild animal populations and humans. These outcomes  can be mediated by epigenetic changes, such as DNA methylation. However,  transgenerational epigenetic inheritance is difficult to study in mammals due to  long generation times and need for ethical practices. We therefore use New  Approach Methodologies, such as responsive invertebrates, to identify the  mechanisms underpinning transgenerational health outcomes.  A powerful species used to understand transgenerational epigenetics is Daphnia  magna. Daphnia are freshwater crustaceans which can be resurrected from  dormant life stages obtained from sediment cores. This PhD will use Daphnia  resurrected from two temporal populations: ~1980s when the lake had high  pollution and the late ~1800s when pollution was lower. These populations will  allow us to test how ancestral exposure effects epigenetic responses to modern  day pollution.  Aim 1: determine if pollution-induced DNA methylation changes can act as  biomarkers, predicting the health of future generations.  Aim 2: determine if these DNA methylation changes are dependent on ancestral  exposure, i.e. genetically mediated through evolutionary processes.  You will be trained in:  -ecotoxicology to carry out chemical exposures, measuring fitness (fecundity,  growth, development time) across multiple generations  -the full pipeline of Nanopore Sequencing (extractions, library preparation,  sequencing, bioinformatic analysis)  -machine learning to integrate DNA methylation and phenotypic data  The last component of your project is dependent on your interests; you can  either pursue further machine learning models, attempt CRISPR/Cas9 DNA  methylation editing to see if epigenetic changes play a causative role in  phenotypic outcomes, validate your biomarkers by resurrecting a new historical  population or carry out fieldwork to test your biomarkers in modern  populations.  Techniques that will be undertaken during the project  - Ecotoxicology using New Approach Methodologies (Daphnia magna)  - Molecular biology: DNA/RNA extraction etc.  - Nanopore sequencing  - Bioinformatic analysis (R / Bash / Python / Machine Learning) | |
| **References** | |
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